

SEQUENCE LISTING

<110> Maliszewski, Charles R.  
Gayle III, Richard B.  
Price, Virginia L.  
Gimpel, Steven D.

<120> Inhibitors of Platelet Activation and Recruitment

<130> 2879-US

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<150> US 60/104,585

<151> 1998-10-16

<150> US 60/107,466

<151> 1998-11-06

<150> US 60/149,010

<151> 1999-08-13

<150> PCT/US99/22955

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<160> 31

<170> PatentIn Ver. 2.0

<210> 1

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aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156

Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile

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20

25

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gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204

Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn

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gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252

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55

60

INS  
A2

0985147-041301

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His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	
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Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	
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tac	ctg	gga	gcc	acg	gca	ggc	atg	cgg	ttg	ctc	agg	atg	gaa	agt	gaa	492
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
			130					135					140			
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Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
		145					150					155				
tac	ccc	ttt	gac	ttc	cag	ggg	gcc	agg	atc	att	act	ggc	caa	gag	gaa	588
Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	
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ggg	gcc	tat	ggc	tgg	att	act	atc	aac	tat	ctg	ctg	ggc	aaa	ttc	agt	636
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
	175				180					185					190	
cag	aaa	aca	agg	tgg	ttc	agc	ata	gtc	cca	tat	gaa	acc	aat	aat	cag	684
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
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gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	ggc	tct	aca	caa	gtc	act	732
Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	
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Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly	
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att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
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acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	
335 340 345 350	
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1164
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	
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atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1212
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
370 375 380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1260
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
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tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr	
415 420 425 430	
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1404
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
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gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
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cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc	1500
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val	
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ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata	1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile	
480 485 490	
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta	1596
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<212> PRT  
<213> Homo sapiens

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Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
35 40 45  
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
50 55 60  
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
65 70 75 80  
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
85 90 95  
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
100 105 110  
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
115 120 125  
Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
130 135 140  
Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
145 150 155 160  
Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
165 170 175  
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190  
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205  
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220  
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240  
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255  
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270

INS  
A2

003544 041301

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
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Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
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<211> 476

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion  
construct of human CD39

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Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln  
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala  
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu  
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu  
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro  
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala  
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys  
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr  
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val  
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg  
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr  
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val  
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys  
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg  
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly  
305 310 315 320

INS  
A2

09835147 041301  
FOETHO 215860

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser  
 325 330 335  
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
 340 345 350  
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
 355 360 365  
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475  
 <210> 4  
 <211> 476  
 <212> PRT  
 <213> Artificial Sequence  
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 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39  
 <220>  
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 <222> (39)  
 <223> Any amino acid, preferably Cys or Ser  
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 20 25 30  
 Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60

09835147.041301







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85 90 95	
tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met	336
100 105 110	
cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp	384
115 120 125	
gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala	432
130 135 140	
agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile	480
145 150 155 160	
aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile	528
165 170 175	
gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu	576
180 185 190	
ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile	624
195 200 205	
gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr	672
210 215 220	
aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	720
225 230 235 240	
tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	768
245 250 255	
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	816
260 265 270	
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	864
275 280 285	
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	912
290 295 300	

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caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag 960
Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
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tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg 1008
Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
                      325                      330                      335

gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca 1056
Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
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gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt 1104
Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
                      355                      360                      365

gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag 1152
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
                      370                      375                      380

aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc 1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385                      390                      395                      400

ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat 1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
                      405                      410                      415

ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac 1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
                      420                      425                      430

atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca 1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
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cct ctc tcc cac tcc acc taa 1365
Pro Leu Ser His Ser Thr
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<211> 454

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion  
construct of human CD39

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Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20                      25                      30

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Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu  
35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val  
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly  
65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg  
85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met  
100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp  
115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala  
130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile  
145 150 155 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile  
165 170 175

Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu  
180 185 190

Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile  
195 200 205

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr  
210 215 220

Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu  
225 230 235 240

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu  
245 250 255

Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser  
260 265 270

Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro  
275 280 285

Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His  
290 295 300

Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln  
305 310 315 320

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly  
325 330 335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser  
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys  
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu  
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu  
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His  
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr  
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Pro Leu Ser His Ser Thr  
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<210> 7

<211> 1437

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fusion  
construct of human CD39

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<221> CDS

<222> (1)..(1434)

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agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys	
20 25 30	
aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac	144
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn	
35 40 45	
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta	192
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg	240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	
65 70 75 80	

cat	caa	gta	gaa	gaa	tgc	agg	gtt	aaa	ggc	cct	gga	atc	tca	aaa	ttt	288
His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	
859095																
gtt	cag	aaa	gta	aat	gaa	ata	ggc	att	tac	ctg	act	gat	tgc	atg	gaa	336
Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	
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aga	gct	agg	gaa	gtg	att	cca	agg	tcc	cag	cac	caa	gag	aca	ccc	gtt	384
Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	
115120125																
tac	ctg	gga	gcc	acg	gca	ggc	atg	cgg	ttg	ctc	agg	atg	gaa	agt	gaa	432
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
130135140																
gag	ttg	gca	gac	agg	gtt	ctg	gat	gtg	gtg	gag	agg	agc	ctc	agc	aac	480
Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
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Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	
165170175																
ggc	gcc	tat	ggc	tgg	att	act	atc	aac	tat	ctg	ctg	ggc	aaa	ttc	agt	576
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
180185190																
cag	aaa	aca	agg	tgg	ttc	agc	ata	gtc	cca	tat	gaa	acc	aat	aat	cag	624
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
195200205																
gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	gcc	tct	aca	caa	gtc	act	672
Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	
210215220																
ttt	gta	ccc	caa	aac	cag	act	atc	gag	tcc	cca	gat	aat	gct	ctg	caa	720
Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	
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Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	
245250255																
tgc	tat	ggg	aag	gat	cag	gca	ctc	tgg	cag	aaa	ctg	gcc	aag	gac	att	816
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	
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cag	gtt	gca	agt	aat	gaa	att	ctc	agg	gac	cca	tgc	ttt	cat	cct	gga	864
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	
275280285																
tat	aag	aag	gta	gtg	aac	gta	agt	gac	ctt	tac	aag	acc	ccc	tgc	acc	912
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
290295300																

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 960  
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly  
 305 310 315 320

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1008  
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
 325 330 335

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1056  
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1104  
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
 355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1152  
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
 370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1200  
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
 385 390 395 400

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1248  
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
 405 410 415

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1296  
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1344  
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
 435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1392  
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
 450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa 1437  
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470 475

<210> 8  
 <211> 478  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 8  
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 1 5 10 15

0508314 041300  
 "041300" 041300

Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	20	25	30
Lys	Thr	Gln	Leu	Thr	Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	35	40	45
Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	50	55	60
Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	65	70	75
His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	85	90	95
Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	100	105	110
Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	115	120	125
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	130	135	140
Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	145	150	155
Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	165	170	175
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	180	185	190
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	195	200	205
Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	210	215	220
Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	225	230	235
Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	245	250	255
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	260	265	270
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	275	280	285
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	290	295	300
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	305	310	315



098347.041301  
TDETHQ"ZTFSEBEO

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn  
325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu  
340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val  
355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val  
370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys  
385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe  
405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr  
420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser  
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile  
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser  
20

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 11  
<211> 43  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 11  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15  
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys  
35 40

<210> 12  
<211> 29  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 12  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15  
Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys  
20 25

<210> 13  
<211> 31  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 13  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15  
Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys  
20 25 30

Sequence 4736

<210> 14  
<211> 87  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 14  
ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
tgtccacacc tctctcccac gagcccc 87

<210> 15  
<211> 87  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 15  
gatcggggct cgtgggagag aggtgtggac aatggttgct cagctgggat catgttggtc 60  
aggttcagca tgtagcccaa agtccag 87

<210> 16  
<211> 740  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (42)..(737)

<400> 16  
cggtagcgct agcgctcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56  
Glu Pro Arg Ser Cys  
1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly  
10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152  
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
25 30 35

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 200  
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
40 45 50

09835147.041301

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	248
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
55 60 65	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	296
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
70 75 80 85	
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	344
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
90 95 100	
aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atg	392
Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met	
105 110 115	
cag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	440
Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
120 125 130	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	488
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
135 140 145	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agg cac atc gcc gtg gag	536
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu	
150 155 160 165	
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	584
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
170 175 180	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	632
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
185 190 195	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	680
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
200 205 210	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	728
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
215 220 225	
ccg ggt aaa tga	740
Pro Gly Lys	
230	

<210> 17  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
 1 5 10 15

Figure 1 consists of 12 sub-diagrams labeled (a) through (l), arranged vertically. Each diagram shows a different stage in the construction of a 3D molecular model. (a) shows a protein structure with a binding site. (b) shows a ligand molecule. (c) shows the ligand docked into the binding site. (d) through (l) show the iterative refinement of the model, including the addition of water molecules and the final optimized structure.

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

18

21

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 19  
aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20  
<211> 24  
<212> PRT  
<213> Mus sp.

<400> 20  
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser  
20

<210> 21  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 21  
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46

<210> 22  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 22  
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46

<210> 23  
<211> 89  
<212> DNA  
<213> Artificial Sequence

<220>  
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oligonucleotide

09835447-044304  
TDETH0-24T52960

<400> 23  
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tgtccacacc tctctcccac tccacctaa 89

<210> 24  
<211> 89  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 24  
ggccttaggt ggagtgggag agaggtgtgg acaatggttg ctcagctggg atcatgttgg 60  
tcaggttcag catgtagccc aaagtccag 89

<210> 25  
<211> 1464  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(1461)

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 25  
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1 5 10 15  
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30  
aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144  
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys  
35 40 45  
acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192  
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
50 55 60  
gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240  
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala  
65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288
Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg	
85 90 95	
gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata	336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile	
100 105 110	
ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca	384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro	
115 120 125	
agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc	432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly	
130 135 140	
atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg	480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu	
145 150 155 160	
gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt	528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly	
165 170 175	
gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act	576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr	
180 185 190	
atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc	624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser	
195 200 205	
ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac	672
Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp	
210 215 220	
ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act	720
Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr	
225 230 235 240	
atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac	768
Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp	
245 250 255	
tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca	816
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala	
260 265 270	
ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att	864
Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile	
275 280 285	
ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta	912
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val	
290 295 300	



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agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt 960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
305                      310                      315                      320

cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc 1008
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
                      325                      330                      335

cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc 1056
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
                      340                      345                      350

cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt 1104
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
                      355                      360                      365

ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca 1152
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
                      370                      375                      380

tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc 1200
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
385                      390                      395                      400

tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag 1248
Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
                      405                      410                      415

gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc 1296
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
                      420                      425                      430

ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc 1344
Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
                      435                      440                      445

cat ttc att ggc aag atc cag ggc agc gac gcc gcc tgg act ttg ggc 1392
His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
                      450                      455                      460

tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc 1440
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
465                      470                      475                      480

aca cct ctc tcc cac tcc acc taa 1464
Thr Pro Leu Ser His Ser Thr
                      485

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<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

0933147-041301

<400> 26

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Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
			20					25					30		
Lys	Thr	Gln	Leu	Thr	Ser	Ser	Gly	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
		35					40					45			
Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu
	50					55					60				
Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala
65					70					75					80
Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg
				85					90					95	
Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile
			100					105					110		
Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro
		115					120					125			
Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly
	130					135					140				
Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu
145					150					155					160
Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly
				165					170					175	
Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr
			180					185					190		
Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser
		195					200					205			
Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp
	210					215					220				
Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr
225					230					235					240
Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp
				245					250					255	
Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala
		260						265					270		
Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile
		275					280					285			
Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val
	290					295					300				

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Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu  
305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys  
325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser  
340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe  
355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr  
370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe  
385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys  
405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser  
420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile  
435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly  
450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser  
465 470 475 480

Thr Pro Leu Ser His Ser Thr  
485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro  
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr  
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly  
50 55 60

Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	65	70	75	80
Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	85	90	95	
Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	100	105	110	
Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	115	120	125	
Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	130	135	140	
Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	145	150	155	160
Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	165	170	175	
Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	180	185	190	
Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	195	200	205	
Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	210	215	220	
Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	225	230	235	240
Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	245	250	255	
Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	260	265	270	
Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	275	280	285	
Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	290	295	300	
Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	305	310	315	320
Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	325	330	335	
Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	340	345	350	
Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	355	360	365	

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Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu  
370 375 380

Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr  
385 390 395 400

Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His  
405 410 415

Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln  
420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn  
435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
450 455 460

<210> 28  
<211> 474  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 28  
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu  
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly  
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys  
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu  
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val  
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu  
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala  
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp  
130 135 140

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Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	
145					150					155					160	
Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	
				165					170						175	
Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	
			180					185					190			
Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	
		195					200					205				
Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	
	210					215					220					
Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	
225					230					235					240	
Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	
				245					250					255		
Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	
			260					265					270			
Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	
		275					280					285				
Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	
	290					295					300					
Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	
305					310					315					320	
Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	
				325					330					335		
Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	
			340					345					350			
Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	
		355					360					365				
Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	
	370					375					380					
Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	
385					390					395					400	
Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	
				405					410					415		
Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	
			420					425					430			
Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	
		435					440					445				

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Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln  
 450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
 construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr  
 20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile  
 35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp  
 50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu  
 65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn  
 85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val  
 100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr  
 115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg  
 130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe  
 145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp  
 165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp  
 180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala  
 195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn  
 210 215 220

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Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly  
 225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp  
 245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn  
 260 265 270

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val  
 275 280 285

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met  
 290 295 300

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln  
 305 310 315 320

Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro  
 325 330 335

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly  
 340 345 350

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn  
 355 360 365

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys  
 370 375 380

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly  
 385 390 395 400

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile  
 405 410 415

Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu  
 420 425 430

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr  
 435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro  
 450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr  
 465 470

<210> 30  
 <211> 463  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion  
 construct of human CD39



09335147 041304

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu  
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser  
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val  
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys  
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met  
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro  
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser  
115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser  
130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu  
145 150 155 160

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe  
165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn  
180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val  
195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu  
210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe  
225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp  
245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro  
260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys  
275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln  
290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe  
305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe  
325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe  
340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys  
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile  
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys  
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe  
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly  
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met  
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr  
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu  
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr  
50 55

115  
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